

SEQUENCE LISTING

<110> Saucier, Caroline
 Park, Morag
 Pawson, Anthony J.
 Lai, Ka-Man

<120> SHC MODULATION AND USES THEREOF

<130> MGU-0024

<150> US 60/447,709

<151> 2003-02-19

<160> 16

<170> PatentIn version 3.1

<210> 1

<211> 3031

<212> DNA

<213> Homo sapiens

<400> 1

gcggtaacct aagctggcag tggcgtgatc cggcaccaaa tcggcccgcg gtgcgtgcgg
 60

agactccatg aggccttga catgaacaag ctgagtggag gcggcgggag caggactcgg
 120

gtggaagggg gccagcttgg gggcgaggag tggacccgcc acgggagctt tgtcaataag
 180

cccacgcggg gctggctgca tcccaacgac aaagtcatgg gaccgggggt ttctacttg
 240

gttcggtaca tgggttgtgt ggaggtctc cagtcaatgc gtgccctgga cttcaacacc
 300

cggactcagg tcaccagga ggccatcagt ctggtgtgtg aggctgtgcc ggggtgctaag
 360

ggggcgacaa ggaggagaaa gccctgtagc cggccgctca gctctatcct ggggaggagt
 420

aacctgaaat ttgctggaat gccaatcact ctcaccgtct ccaccagcag cctcaacctc
 480

atggccgcag actgcaaaca gatcatcgcc aaccaccaca tgcaatctat ctcatttgca
 540

tccggcgggg atccggacac agccgagtat gtcgcctatg ttgcaaaga ccctgtgaat
 600

cagagagcct gccacattct ggagtgtccc gaagggttg cccaggatgt catcagcacc
 660

attggccagg ccttcgagtt gcgcttcaaa caatacctca ggaacccacc caaactggtc
 720

acccctcatg acaggatggc tggctttgat ggctcagcat gggatgagga ggaggaagag
 780

ccacctgacc atcagtacta taatgacttc ccggggaagg aacccccctt ggggggggtg
 840

gtagacatga ggcttcggga aggagccgct ccaggggctg ctcgaccac tgcaccaat
 900

gccagaccc ccagccactt gggagctaca ttgcctgtag gacagcctgt tgggggagat
 960

ccagaagtcc gcaaacagat gccacctcca ccaccctgtc caggcagaga gctttttgat
 1020

gatccctcct atgtcaacgt ccagaaccta gacaaggccc ggcaagcagt ggggtggtgct
 1080

gggcccccca atcctgctat caatggcagt gcaccccggt acctgtttga catgaagccc
 1140

ttggaagatg ctcttcgggt gcctccacct cccagtcgg tgtccatggc tgagcagctc
 1200

cgaggggagc cctggttcca tgggaagctg agccggcggg aggctgaggc actgctgcag
 1260

ctcaatgggg acttcttgggt acgggagagc acgaccacac ctggccagta tgtgctcact
 1320

ggcttgacga gtgggcagcc taagcatttg ctactggtgg accctgaggg tgtggttcgg
 1380

actaaggatc accgctttga aagtgtcagt caccttatca gctaccacat ggacaatcac
 1440

ttgcccacat tctctgcggg cagcgaactg tgtctacagc aacctgtgga gcggaaactg
 1500

tgatctgccc tagcgtcttc ttccagaaga tgccctccaa tcctttccac cctattccct
 1560

aactctcggg acctcgtttg ggagtgttct gtgggcttgg ccttgtgtca gagctgggag
 1620

tagcatggac tctgggtttc atatccagct gaggagagg gtttgagtca aaagcctggg
 1680

tgagaatcct gcctctcccc aaacattaat caccaaagta ttaatgtaca gagtggcccc
 1740

tcacctgggc ctttctgtg ccaacctgat gcccttccc caagaagggt agtgcttgtc
 1800

atggaaaatg tcctgtggtg acaggcccag tggaacagtc acccttctgg gcaaggggga
 1860

acaaatcaca cctctgggct tcagggtatc ccagaccct ctcaacaccc gccccccca
1920

tgtttaaact ttgtgccttt gaccatctct taggtctaata gatattttat gcaaacagtt
1980

cttggacccc tgaattcttc aatgacaggg atgccaacac cttcttggct tctgggacct
2040

gtgttcttgc tgagcacct ctccggtttg ggttgggata acagaggcag gagtggcagc
2100

tgtccctct ccctggggat atgcaacct tagagattgc ccagagccc cactcccggc
2160

caggcgggag atggaccct cccttgccta gtgcctctg gccggggccc ctcaccccaa
2220

ggggtctgta tatactttc ataaggcctg cctcccatg ttgcatgcct atgtactctg
2280

cgccaaagt cagcccttc tctgaagcc tctgcctgc ctccctttct gggagggcgg
2340

ggtgggggtg actgaatttg ggctcttgt acagttaact ctcccagggt gattttgtgg
2400

aggtgagaaa aggggcattg agactataaa gcagtagaca atccccacat accatctgta
2460

gagttggaac tgcatcttt taaagtttta tatgcatata ttttagggct gctagactta
2520

ctttcctatt ttcttttcca ttgcttattc ttgagcaca aatgataatc aattattaca
2580

tttatacatc acctttttga cttttccaag cccttttaca gctcttggca ttttcctcgc
2640

ctaggcctgt gaggtaactg ggatcgacc ttttatacca gagacctgag gcagatgaaa
2700

tttatttcca tctaggacta gaaaaacttg ggtctcttac cgcgagactg agaggcagaa
2760

gtcagcccga atgcctgtca gtttcatgga ggggaaacgc aaaacctgca gttcctgagt
2820

accttctaca ggcccggccc agcctaggcc cgggggtggc acaccacagc aagccggccc
2880

cccctctttt ggcttctgtg ataagggaga gttgaccgtt ttcctcctgg cctccttttg
2940

ctgtttggat gtttccacgg gtctcaacta taccaaaggg aaaactcttc attaaagtcc
3000

cgtatttctt ctaaaaaaaaa aaaaaaaaaa a
3031

<210> 2
 <211> 473
 <212> PRT
 <213> Homo sapiens

<400> 2

Met Asn Lys Leu Ser Gly Gly Gly Gly Arg Arg Thr Arg Val Glu Gly
 1 5 10 15

Gly Gln Leu Gly Gly Glu Glu Trp Thr Arg His Gly Ser Phe Val Asn
 20 25 30

Lys Pro Thr Arg Gly Trp Leu His Pro Asn Asp Lys Val Met Gly Pro
 35 40 45

Gly Val Ser Tyr Leu Val Arg Tyr Met Gly Cys Val Glu Val Leu Gln
 50 55 60

Ser Met Arg Ala Leu Asp Phe Asn Thr Arg Thr Gln Val Thr Arg Glu
 65 70 75 80

Ala Ile Ser Leu Val Cys Glu Ala Val Pro Gly Ala Lys Gly Ala Thr
 85 90 95

Arg Arg Arg Lys Pro Cys Ser Arg Pro Leu Ser Ser Ile Leu Gly Arg
 100 105 110

Ser Asn Leu Lys Phe Ala Gly Met Pro Ile Thr Leu Thr Val Ser Thr
 115 120 125

Ser Ser Leu Asn Leu Met Ala Ala Asp Cys Lys Gln Ile Ile Ala Asn
 130 135 140

His His Met Gln Ser Ile Ser Phe Ala Ser Gly Gly Asp Pro Asp Thr
 145 150 155 160

Ala Glu Tyr Val Ala Tyr Val Ala Lys Asp Pro Val Asn Gln Arg Ala
 165 170 175

Cys His Ile Leu Glu Cys Pro Glu Gly Leu Ala Gln Asp Val Ile Ser
 180 185 190

Thr Ile Gly Gln Ala Phe Glu Leu Arg Phe Lys Gln Tyr Leu Arg Asn
 195 200 205

Pro Pro Lys Leu Val Thr Pro His Asp Arg Met Ala Gly Phe Asp Gly
 210 215 220

Ser Ala Trp Asp Glu Glu Glu Glu Glu Pro Pro Asp His Gln Tyr Tyr
 225 230 235 240

Asn Asp Phe Pro Gly Lys Glu Pro Pro Leu Gly Gly Val Val Asp Met
 245 250 255

Arg Leu Arg Glu Gly Ala Ala Pro Gly Ala Ala Arg Pro Thr Ala Pro
 260 265 270

Asn Ala Gln Thr Pro Ser His Leu Gly Ala Thr Leu Pro Val Gly Gln
 275 280 285

Pro Val Gly Gly Asp Pro Glu Val Arg Lys Gln Met Pro Pro Pro Pro
 290 295 300

Pro Cys Pro Gly Arg Glu Leu Phe Asp Asp Pro Ser Tyr Val Asn Val
 305 310 315 320

Gln Asn Leu Asp Lys Ala Arg Gln Ala Val Gly Gly Ala Gly Pro Pro
 325 330 335

Asn Pro Ala Ile Asn Gly Ser Ala Pro Arg Asp Leu Phe Asp Met Lys
 340 345 350

Pro Phe Glu Asp Ala Leu Arg Val Pro Pro Pro Pro Gln Ser Val Ser
 355 360 365

Met Ala Glu Gln Leu Arg Gly Glu Pro Trp Phe His Gly Lys Leu Ser
 370 375 380

Arg Arg Glu Ala Glu Ala Leu Leu Gln Leu Asn Gly Asp Phe Leu Val
 385 390 395 400

Arg Glu Ser Thr Thr Thr Pro Gly Gln Tyr Val Leu Thr Gly Leu Gln
 405 410 415

Ser Gly Gln Pro Lys His Leu Leu Leu Val Asp Pro Glu Gly Val Val
 420 425 430

Arg Thr Lys Asp His Arg Phe Glu Ser Val Ser His Leu Ile Ser Tyr
 435 440 445

His Met Asp Asn His Leu Pro Ile Ile Ser Ala Gly Ser Glu Leu Cys
 450 455 460

Leu Gln Gln Pro Val Glu Arg Lys Leu
 465 470

<210> 3
 <211> 3664
 <212> DNA
 <213> Homo sapiens

<400> 3
 atggggcctg aaactgtctg ggtctgagct ggggagcgga agccacttgt ccctctccct
 60
 cccagaggact tctgtgactc ctgggccaca gaggtccaac cagggttaagg gcctggggat
 120
 accccctgcc tggccccctt gcccaaactg gcaggggggc caggctgggc agcagcccct
 180
 ctttcacctc aactatggat ctctgcccc ccaagcccaa gtacaatcca ctccggaatg
 240
 agtctctgtc atcgctggag gaaggggctt ctgggtccac cccccggag gagctgcctt
 300
 ccccatcagc ttcatccctg gggcccatcc tgctctctct gcctggggac gatagtccca
 360
 ctaccctgtg ctcttcttc ccccgatga gcaacctgag gctggccaac ccggctgggg
 420
 ggcgcccagg gtctaagggg gagccaggaa gggcagctga tgatggggag gggatcgatg
 480
 gggcagccat gccagagtca ggccccctac cctcctcca ggacatgaac aagctgagtg
 540
 gaggcggcgg gcgcaggact cgggtggaag ggggccagct tgggggcgag gagtggaccc
 600
 gccacgggag ctttgtcaat aagcccacgc ggggctggct gcatcccaac gacaaagtca
 660
 tgggacccgg ggtttcctac ttggttcggt acatggggtg tgtggaggtc ctccagtcaa
 720
 tgcgtgccct ggacttcaac acccggactc aggtcaccag ggaggccatc agtctgggtg
 780
 gtgaggctgt gccgggtgct aagggggcga caaggaggag aaagccctgt agccgcccgc
 840
 tcagctctat cctggggagg agtaacctga aatttgctgg aatgccaatc actctcaccg
 900

tctccaccag cagcctcaac ctcatggccg cagactgcaa acagatcatc gccaaaccacc
960

acatgcaatc tatctcattt gcatccggcg gggatccgga cacagccgag tatgtcgcct
1020

atgttgccaa agaccctgtg aatcagagag cctgccacat tctggagtgt cccgaagggc
1080

ttgcccagga tgtcatcagc accattggcc aggccttcga gttgcgcttc aaacaataacc
1140

tcaggaaccc acccaaactg gtcacccctc atgacaggat ggctggcttt gatggctcag
1200

catgggatga ggaggaggaa gagccacctg accatcagta ctataatgac ttcccgggga
1260

aggaaccccc cttggggggg gtggtagaca tgaggcttcg ggaaggagcc gctccagggg
1320

ctgctcgacc cactgcaccc aatgccaga ccccagcca cttgggagct acattgcctg
1380

taggacagcc tgttggggga gatccagaag tccgcaaaca gatgccacct ccaccacct
1440

gtccaggcag agagcttttt gatgatccct cctatgtcaa cgtccagaac ctagacaagg
1500

cccggcaagc agtgggtggt gctgggcccc ccaatcctgc tatcaatggc agtgcacccc
1560

gggacctgtt tgacatgaag cccttcgaag atgctcttcg ggtgcctcca cctccccagt
1620

cggtgtccat ggctgagcag ctccgagggg agccctgggt ccatgggaag ctgagccggc
1680

gggaggctga ggcactgctg cagctcaatg gggacttctt ggtacgggag agcacgacca
1740

cacctggcca gtatgtgctc actggcttgc agagtgggca gcctaagcat ttgctactgg
1800

tggaccctga ggggtgtggt cggactaagg atcaccgctt tgaaagtgtc agtcacctta
1860

tcagctacca catggacaat cacttgccca tcatctctgc gggcagcgaa ctgtgtctac
1920

agcaacctgt ggagcgga aa ctgtgatctg ccctagcgct ctcttccaga agatgcctc
1980

caatcctttc caccctattc cctaactctc gggacctcgt ttgggagtgt tctgtgggct
2040

tggccttggt tcagagctgg gagtagcatg gactctgggt tcatatcca gctgagtga
2100

agggtttgag tcaaaagcct gggtgagaat cctgcctctc cccaaacatt aatcacaaa
2160

gtattaatgt acagagtggc ccctcacctg ggcctttcct gtgccaacct gatgccctt
2220

cccaagaag gtgagtgctt gtcattgaaa atgtcctgtg gtgacaggcc cagtgaaca
2280

gtcacccttc tgggcaagg ggaacaaatc acacctctgg gcttcagggt atcccagacc
2340

cctctcaaca cccgcccccc ccattgttaa actttgtgcc ttgaccatc tcttaggtct
2400

aatgatattt tatgcaaaca gttcttggac ccctgaattc ttcaatgaca gggatgcaa
2460

caccttcttg gcttctggga cctgtgttct tgetgagcac cctctccggt ttgggttggg
2520

ataacagagg caggagtggc agctgtcccc tctccctggg gatatgcaac ccttagagat
2580

tgccccagag cccactccc ggccaggcgg gagatggacc cctcccttgc tcagtgcctc
2640

ctggccgggg cccctcacc caaggggtct gtatatacat ttcataaggc ctgccctccc
2700

atgttgcatg cctatgtact ctgcgcaaaa gtgcagccct tctcctgaa gcctctgcc
2760

tgcctccctt tctgggaggg cgggggtggg gtgactgaat ttgggcctct tgtacagtta
2820

actctcccag gtggattttg tggaggtgag aaaaggggca ttgagactat aaagcagtag
2880

acaatcccca cataccatct gtagagtgg aactgcattc ttttaaagtt ttatatgat
2940

atattttagg gctgctagac ttactttcct attttctttt ccattgctta ttcttgagca
3000

caaatgata atcaattatt acatttatac atcacctttt tgacttttcc aagccctttt
3060

acagctcttg gcattttcct cgcctaggcc tgtgaggtaa ctgggatcgc accttttata
3120

ccagagacct gaggcagatg aaatttattt ccatttagga ctagaaaaac ttgggtctct
3180

taccgcgaga ctgagaggca gaagtcagcc cgaatgcctg tcagtttcat ggaggggaaa
3240

cgcaaaacct gcagttcctg agtaccttct acaggcccgg cccagcctag gcccggggtg
3300

gccacaccac agcaagccgg cccccctct tttggccttg tggataaggg agagttgacc
3360

gttttcatcc tggcctcctt ttgctgtttg gatgtttcca cgggtctcac ttatacctaa
3420

gggaaaactc ttcattaaag tccgtatttc ttctaaaaaa aaaaaaaaaa aaatacattt
3480

atacatcacc tttttgactt ttccaagccc ttttacagct cttggcattt tcctcgcta
3540

ggcctgtgag gtaactggga tcgcaccttt tataccagag acctgaggca gatgaaattt
3600

atttccatct aggactagaa aaacttgggt ctcttaccgc gagactgaga ggcagaagtc
3660

agcc
3664

<210> 4
<211> 583
<212> PRT
<213> Homo sapiens

<400> 4

Met Asp Leu Leu Pro Pro Lys Pro Lys Tyr Asn Pro Leu Arg Asn Glu
1 5 10 15

Ser Leu Ser Ser Leu Glu Glu Gly Ala Ser Gly Ser Thr Pro Pro Glu
20 25 30

Glu Leu Pro Ser Pro Ser Ala Ser Ser Leu Gly Pro Ile Leu Pro Pro
35 40 45

Leu Pro Gly Asp Asp Ser Pro Thr Thr Leu Cys Ser Phe Phe Pro Arg
50 55 60

Met Ser Asn Leu Arg Leu Ala Asn Pro Ala Gly Gly Arg Pro Gly Ser
65 70 75 80

Lys Gly Glu Pro Gly Arg Ala Ala Asp Asp Gly Glu Gly Ile Asp Gly
85 90 95

Ala Ala Met Pro Glu Ser Gly Pro Leu Pro Leu Leu Gln Asp Met Asn
100 105 110

Lys Leu Ser Gly Gly Gly Gly Arg Arg Thr Arg Val Glu Gly Gly Gln
115 120 125

Leu Gly Gly Glu Glu Trp Thr Arg His Gly Ser Phe Val Asn Lys Pro
 130 135 140

Thr Arg Gly Trp Leu His Pro Asn Asp Lys Val Met Gly Pro Gly Val
 145 150 155 160

Ser Tyr Leu Val Arg Tyr Met Gly Cys Val Glu Val Leu Gln Ser Met
 165 170 175

Arg Ala Leu Asp Phe Asn Thr Arg Thr Gln Val Thr Arg Glu Ala Ile
 180 185 190

Ser Leu Val Cys Glu Ala Val Pro Gly Ala Lys Gly Ala Thr Arg Arg
 195 200 205

Arg Lys Pro Cys Ser Arg Pro Leu Ser Ser Ile Leu Gly Arg Ser Asn
 210 215 220

Leu Lys Phe Ala Gly Met Pro Ile Thr Leu Thr Val Ser Thr Ser Ser
 225 230 235 240

Leu Asn Leu Met Ala Ala Asp Cys Lys Gln Ile Ile Ala Asn His His
 245 250 255

Met Gln Ser Ile Ser Phe Ala Ser Gly Gly Asp Pro Asp Thr Ala Glu
 260 265 270

Tyr Val Ala Tyr Val Ala Lys Asp Pro Val Asn Gln Arg Ala Cys His
 275 280 285

Ile Leu Glu Cys Pro Glu Gly Leu Ala Gln Asp Val Ile Ser Thr Ile
 290 295 300

Gly Gln Ala Phe Glu Leu Arg Phe Lys Gln Tyr Leu Arg Asn Pro Pro
 305 310 315 320

Lys Leu Val Thr Pro His Asp Arg Met Ala Gly Phe Asp Gly Ser Ala
 325 330 335

Trp Asp Glu Glu Glu Glu Glu Pro Pro Asp His Gln Tyr Tyr Asn Asp
 340 345 350

Phe Pro Gly Lys Glu Pro Pro Leu Gly Gly Val Val Asp Met Arg Leu
 355 360 365

Arg Glu Gly Ala Ala Pro Gly Ala Ala Arg Pro Thr Ala Pro Asn Ala
 370 375 380

Gln Thr Pro Ser His Leu Gly Ala Thr Leu Pro Val Gly Gln Pro Val
 385 390 395 400

Gly Gly Asp Pro Glu Val Arg Lys Gln Met Pro Pro Pro Pro Pro Cys
 405 410 415

Pro Gly Arg Glu Leu Phe Asp Asp Pro Ser Tyr Val Asn Val Gln Asn
 420 425 430

Leu Asp Lys Ala Arg Gln Ala Val Gly Gly Ala Gly Pro Pro Asn Pro
 435 440 445

Ala Ile Asn Gly Ser Ala Pro Arg Asp Leu Phe Asp Met Lys Pro Phe
 450 455 460

Glu Asp Ala Leu Arg Val Pro Pro Pro Pro Gln Ser Val Ser Met Ala
 465 470 475 480

Glu Gln Leu Arg Gly Glu Pro Trp Phe His Gly Lys Leu Ser Arg Arg
 485 490 495

Glu Ala Glu Ala Leu Leu Gln Leu Asn Gly Asp Phe Leu Val Arg Glu
 500 505 510

Ser Thr Thr Thr Pro Gly Gln Tyr Val Leu Thr Gly Leu Gln Ser Gly
 515 520 525

Gln Pro Lys His Leu Leu Leu Val Asp Pro Glu Gly Val Val Arg Thr
 530 535 540

Lys Asp His Arg Phe Glu Ser Val Ser His Leu Ile Ser Tyr His Met
 545 550 555 560

Asp Asn His Leu Pro Ile Ile Ser Ala Gly Ser Glu Leu Cys Leu Gln
 565 570 575

Gln Pro Val Glu Arg Lys Leu
 580

<210> 5
 <211> 1879
 <212> DNA

<213> Homo sapiens

<400> 5

agctatgaat ctcttgcccc ccaagcccaa gtacaatcca ctccggaatg agtctctgtc
60

atcgatggag gaaggggctt ctgggtccac cccccggag gagctgcctt cccaccagc
120

ttcatccctg gggcccatcc tgcctcctct gcctggggac gatagtccca ctaccctgtg
180

ctccttcttc ccccgatga gcaacctgag gctggccaac ccggctgggg ggcgcccagg
240

gtctaagggg gagccaggaa gggcagctga tgatggggag gggatcgtag gggcagccat
300

gccagactca ggccccctac ccctcctcca ggacatgaac aagctgagtg gaggcggcgg
360

gcgcaggact cgggtggaag ggggccagct tgggggcgag gagtggacct gccacgggag
420

ctttgtcaat aagcccacgc ggggctggct gcatcccaac gacaaagtca tgggaccggg
480

ggtttcctac ttggttcggt acatggggtg tgtggaggtc ctccagtcaa tgcgtgcct
540

ggacttcaac acccggaactc aggtcaccag ggaggccatc agtctggtgt gtgaggctgt
600

gccgggtgct aagggggcga caaggaggag aaagccctgt agccgccgc tcagctctat
660

cctggggagg agtaacctga aatttgctgg aatgccaatc actctcaccg tctccaccag
720

cagcctcaac ctcatggcg cagactgcaa acagatcatc gcccaaccacc acatgcaatc
780

tatctcattt gcatccggcg gggatccgga cacagccgag tatgtcgctt atgttgccaa
840

agaccctgtg aatcagagag cctgccacat totggagtgt cccgaagggc ttgccaggag
900

tgtcatcagc accattggcc aggccttcga gttgcgcttc aaacaatacc tcaggaaccc
960

acccaaactg gtcaccctc atgacaggat ggctggcttt gatggctcag catgggatga
1020

ggaggaggaa gagccacctg accatcagta ctataatgac ttcccgggga aggaaccccc
1080

cttggggggg gtggtagaca tgaggcttcg ggaaggagcc gctccagggg ctgctcgacc
1140

cactgcaccc aatgcccaga cccccagcca cttgggagct acattgcctg taggacagcc
1200

tgttggggga gatccagaag tccgcaaaca gatgccacct ccaccaccct gtccaggcag
1260

agagcttttt gatgatccct cctatgtcaa cgtccagaac ctagacaagg cccggcaagc
1320

agtgggtggt gctgggcccc ccaatcctgc tatcaatggc agtgcacccc gggacctgtt
1380

tgacatgaag cccttcgaag atgctcttcg ggtgcctcca cctccccagt cgggtgtccat
1440

ggctgagcag ctccgagggg agccctgggt ccatgggaag ctgagccggc gggaggctga
1500

ggcactgctg cagctcaatg gggacttctt ggtacgggag agcacgacca cacctggcca
1560

gtatgtgctc actggcttgc agagtgggca gcctaagcat ttgctactgg tggaccctga
1620

gggtgtgggt cggactaagg atcacgctt tgaaagtgtc agtcacctta tcagctacca
1680

catggacaat cacttgccca tcattctctgc gggcagcgaa ctgtgtctac agcaacctgt
1740

ggagcggaaa ctgtgatctg ccctagcgct ctcttcacaga agatgccctc caatcctttc
1800

caccctattc cctaactctc gggacctcgt ttgggagtgt tctgtgggct tggccttgtg
1860

tcagagctgg gagtagcat
1879

<210> 6

<211> 583

<212> PRT

<213> Homo sapiens

<400> 6

Met Asn Leu Leu Pro Pro Lys Pro Lys Tyr Asn Pro Leu Arg Asn Glu
1 5 10 15

Ser Leu Ser Ser Met Glu Glu Gly Ala Ser Gly Ser Thr Pro Pro Glu
20 25 30

Glu Leu Pro Ser Pro Pro Ala Ser Ser Leu Gly Pro Ile Leu Pro Pro
35 40 45

Leu Pro Gly Asp Asp Ser Pro Thr Thr Leu Cys Ser Phe Phe Pro Arg

					14										
50					55					60					
Met 65	Ser	Asn	Leu	Arg	Leu 70	Ala	Asn	Pro	Ala	Gly 75	Gly	Arg	Pro	Gly	Ser 80
Lys	Gly	Glu	Pro	Gly 85	Arg	Ala	Ala	Asp	Asp 90	Gly	Glu	Gly	Ile	Val 95	Gly
Ala	Ala	Met	Pro 100	Asp	Ser	Gly	Pro	Leu 105	Pro	Leu	Leu	Gln	Asp 110	Met	Asn
Lys	Leu	Ser 115	Gly	Gly	Gly	Gly	Arg 120	Arg	Thr	Arg	Val	Glu 125	Gly	Gly	Gln
Leu	Gly 130	Gly	Glu	Glu	Trp	Thr 135	Arg	His	Gly	Ser	Phe 140	Val	Asn	Lys	Pro
Thr 145	Arg	Gly	Trp	Leu	His 150	Pro	Asn	Asp	Lys	Val 155	Met	Gly	Pro	Gly	Val 160
Ser	Tyr	Leu	Val	Arg 165	Tyr	Met	Gly	Cys	Val 170	Glu	Val	Leu	Gln	Ser 175	Met
Arg	Ala	Leu	Asp 180	Phe	Asn	Thr	Arg	Thr 185	Gln	Val	Thr	Arg	Glu 190	Ala	Ile
Ser	Leu	Val 195	Cys	Glu	Ala	Val	Pro 200	Gly	Ala	Lys	Gly	Ala 205	Thr	Arg	Arg
Arg	Lys 210	Pro	Cys	Ser	Arg	Pro 215	Leu	Ser	Ser	Ile	Leu 220	Gly	Arg	Ser	Asn
Leu 225	Lys	Phe	Ala	Gly	Met 230	Pro	Ile	Thr	Leu	Thr 235	Val	Ser	Thr	Ser	Ser 240
Leu	Asn	Leu	Met	Ala 245	Ala	Asp	Cys	Lys	Gln 250	Ile	Ile	Ala	Asn	His 255	His
Met	Gln	Ser	Ile 260	Ser	Phe	Ala	Ser	Gly 265	Gly	Asp	Pro	Asp	Thr 270	Ala	Glu
Tyr	Val	Ala 275	Tyr	Val	Ala	Lys	Asp 280	Pro	Val	Asn	Gln	Arg 285	Ala	Cys	His
Ile	Leu	Glu	Cys	Pro	Glu	Gly	Leu	Ala	Gln	Asp	Val	Ile	Ser	Thr	Ile

290		295		300														
Gly	Gln	Ala	Phe	Glu	Leu	Arg	Phe	Lys	Gln	Tyr	Leu	Arg	Asn	Pro	Pro			
305					310					315					320			
Lys	Leu	Val	Thr	Pro	His	Asp	Arg	Met	Ala	Gly	Phe	Asp	Gly	Ser	Ala			
				325					330					335				
Trp	Asp	Glu	Glu	Glu	Glu	Glu	Pro	Pro	Asp	His	Gln	Tyr	Tyr	Asn	Asp			
			340					345						350				
Phe	Pro	Gly	Lys	Glu	Pro	Pro	Leu	Gly	Gly	Val	Val	Asp	Met	Arg	Leu			
		355					360					365						
Arg	Glu	Gly	Ala	Ala	Pro	Gly	Ala	Ala	Arg	Pro	Thr	Ala	Pro	Asn	Ala			
	370					375					380							
Gln	Thr	Pro	Ser	His	Leu	Gly	Ala	Thr	Leu	Pro	Val	Gly	Gln	Pro	Val			
385					390					395					400			
Gly	Gly	Asp	Pro	Glu	Val	Arg	Lys	Gln	Met	Pro	Pro	Pro	Pro	Pro	Cys			
				405					410					415				
Pro	Gly	Arg	Glu	Leu	Phe	Asp	Asp	Pro	Ser	Tyr	Val	Asn	Val	Gln	Asn			
			420					425					430					
Leu	Asp	Lys	Ala	Arg	Gln	Ala	Val	Gly	Gly	Ala	Gly	Pro	Pro	Asn	Pro			
		435				440						445						
Ala	Ile	Asn	Gly	Ser	Ala	Pro	Arg	Asp	Leu	Phe	Asp	Met	Lys	Pro	Phe			
450						455					460							
Glu	Asp	Ala	Leu	Arg	Val	Pro	Pro	Pro	Pro	Gln	Ser	Val	Ser	Met	Ala			
465					470					475					480			
Glu	Gln	Leu	Arg	Gly	Glu	Pro	Trp	Phe	His	Gly	Lys	Leu	Ser	Arg	Arg			
				485				490						495				
Glu	Ala	Glu	Ala	Leu	Leu	Gln	Leu	Asn	Gly	Asp	Phe	Leu	Val	Arg	Glu			
			500					505					510					
Ser	Thr	Thr	Thr	Pro	Gly	Gln	Tyr	Val	Leu	Thr	Gly	Leu	Gln	Ser	Gly			
		515					520					525						
Gln	Pro	Lys	His	Leu	Leu	Leu	Val	Asp	Pro	Glu	Gly	Val	Val	Arg	Thr			

530

535

540

Lys Asp His Arg Phe Glu Ser Val Ser His Leu Ile Ser Tyr His Met
 545 550 555 560

Asp Asn His Leu Pro Ile Ile Ser Ala Gly Ser Glu Leu Cys Leu Gln
 565 570 575

Gln Pro Val Glu Arg Lys Leu
 580

<210> 7

<211> 1462

<212> DNA

<213> Mus musculus

<400> 7

cggaaccaga tcggcccgcg gtgcggtgcg gagactccat gagaccctgg acatgaacaa
 60

gctgagtgga ggcgggcgggc gcaggactcg ggtagaaggg ggccagctgg ggggcgagga
 120

gtggaccaga cacgggagct ttgtcaataa gcccacacga ggctggctgc atcccaacga
 180

caaagtcattg ggacctgggg tttctactt ggttcggtac atgggctgtg tggaggtctt
 240

acagtcaatg cgagcccttg acttcaatac ccggactcag gtcaccaggg aggccatcag
 300

tttggtgtgt gaagctgtgc ctggtgccaa aggggcgaca aggaggagaa agccttgtag
 360

ccgcccactc agtccatcc tggggaggag taacctgaag ttgctggaa tgccaatcac
 420

tctcactgtg tctaccagca gccttaacct catggcagcc gactgcaaac agatcattgc
 480

caaccatcac atgcaatcta tctctttcgc gtccgggtggg gatccggaca cagctgagta
 540

tggtgcctat gttgcaaag accctgtgaa tcagagagcc tgccatatcc tggagtgtcc
 600

tgaagggctt gctcaggatg tcatcagcac catcgggcag gcctttgagt tgcgcttcaa
 660

acagtatctc aggaatccac cgaagctggg cccccccat gacaggatgg ctggctttga
 720

tggctcagct tgggatgagg aggaagaaga gcccctgac catcagtact acaatgactt
 780

tccaggggaag gaacccccctc ttggtggggt ggtagatatg aggcttcggg aaggggctgc
840

tcgacccact ctgcctagtgc ccagatgtc cagccacttg ggagctacac tgcctatagg
900

gcagcatgct gcaggagacc atgaagtccg taaacagatg ttgcctccgc cgccttgccc
960

aggcagagaa ctcttcgatg acccctccta tgtcaacatc cagaatctag acaaggcccg
1020

gcaggctggg ggtggggctg ggccccaaa tccttctctt aatggcagtgc cccccgaga
1080

cctttttgac atgaagccct ttgaagatgc acttcgggtg ccacccccac cgcagtccat
1140

gtccatggct gagcagctgc aaggggagcc ctggttccac gggaagctga gccggagggg
1200

ggccgagggc ctgctgcagc tcaatgggtga cttcttggtg cgagagagca cgaccacgcc
1260

tggccagtat gtgctcactg gcctgcagag tgggcagccc aagcacttgc tgctggtgga
1320

ccctgaaggt gtggttcgga caaaggatca ccgctttgag agtgtcagtc acctgatcag
1380

ctaccacatg gacaatcact tgcccatcat ctctgcgggc agcgaactgt gcctacagca
1440

accctgggat cggaaagtgt ga
1462

<210> 8

<211> 469

<212> PRT

<213> Mus musculus

<400> 8

Met Asn Lys Leu Ser Gly Gly Gly Gly Arg Arg Thr Arg Val Glu Gly
1 5 10 15

Gly Gln Leu Gly Gly Glu Glu Trp Thr Arg His Gly Ser Phe Val Asn
20 25 30

Lys Pro Thr Arg Gly Trp Leu His Pro Asn Asp Lys Val Met Gly Pro
35 40 45

Gly Val Ser Tyr Leu Val Arg Tyr Met Gly Cys Val Glu Val Leu Gln
50 55 60

Ser	Met	Arg	Ala	Leu	Asp	Phe	Asn		Thr	Arg	Thr	Gln	Val	Thr	Arg	Glu
65					70				75						80	
Ala	Ile	Ser	Leu	Val	Cys	Glu	Ala	Val	Pro	Gly	Ala	Lys	Gly	Ala	Thr	
			85						90					95		
Arg	Arg	Arg	Lys	Pro	Cys	Ser	Arg	Pro	Leu	Ser	Ser	Ile	Leu	Gly	Arg	
			100					105					110			
Ser	Asn	Leu	Lys	Phe	Ala	Gly	Met	Pro	Ile	Thr	Leu	Thr	Val	Ser	Thr	
		115					120					125				
Ser	Ser	Leu	Asn	Leu	Met	Ala	Ala	Asp	Cys	Lys	Gln	Ile	Ile	Ala	Asn	
		130				135					140					
His	His	Met	Gln	Ser	Ile	Ser	Phe	Ala	Ser	Gly	Gly	Asp	Pro	Asp	Thr	
145					150					155					160	
Ala	Glu	Tyr	Val	Ala	Tyr	Val	Ala	Lys	Asp	Pro	Val	Asn	Gln	Arg	Ala	
				165					170					175		
Cys	His	Ile	Leu	Glu	Cys	Pro	Glu	Gly	Leu	Ala	Gln	Asp	Val	Ile	Ser	
			180					185					190			
Thr	Ile	Gly	Gln	Ala	Phe	Glu	Leu	Arg	Phe	Lys	Gln	Tyr	Leu	Arg	Asn	
		195					200					205				
Pro	Pro	Lys	Leu	Val	Thr	Pro	His	Asp	Arg	Met	Ala	Gly	Phe	Asp	Gly	
		210				215					220					
Ser	Ala	Trp	Asp	Glu	Glu	Glu	Glu	Glu	Pro	Pro	Asp	His	Gln	Tyr	Tyr	
225				230					235						240	
Asn	Asp	Phe	Pro	Gly	Lys	Glu	Pro	Pro	Leu	Gly	Gly	Val	Val	Asp	Met	
				245					250					255		
Arg	Leu	Arg	Glu	Gly	Ala	Ala	Arg	Pro	Thr	Leu	Pro	Ser	Ala	Gln	Met	
			260					265					270			
Ser	Ser	His	Leu	Gly	Ala	Thr	Leu	Pro	Ile	Gly	Gln	His	Ala	Ala	Gly	
		275					280					285				
Asp	His	Glu	Val	Arg	Lys	Gln	Met	Leu	Pro	Pro	Pro	Pro	Cys	Pro	Gly	
		290				295					300					

Arg Glu Leu Phe Asp Asp Pro Ser Tyr Val Asn Ile Gln Asn Leu Asp
 305 310 315 320

Lys Ala Arg Gln Ala Gly Gly Gly Ala Gly Pro Pro Asn Pro Ser Leu
 325 330 335

Asn Gly Ser Ala Pro Arg Asp Leu Phe Asp Met Lys Pro Phe Glu Asp
 340 345 350

Ala Leu Arg Val Pro Pro Pro Pro Gln Ser Met Ser Met Ala Glu Gln
 355 360 365

Leu Gln Gly Glu Pro Trp Phe His Gly Lys Leu Ser Arg Arg Glu Ala
 370 375 380

Glu Ala Leu Leu Gln Leu Asn Gly Asp Phe Leu Val Arg Glu Ser Thr
 385 390 395 400

Thr Thr Pro Gly Gln Tyr Val Leu Thr Gly Leu Gln Ser Gly Gln Pro
 405 410 415

Lys His Leu Leu Leu Val Asp Pro Glu Gly Val Val Arg Thr Lys Asp
 420 425 430

His Arg Phe Glu Ser Val Ser His Leu Ile Ser Tyr His Met Asp Asn
 435 440 445

His Leu Pro Ile Ile Ser Ala Gly Ser Glu Leu Cys Leu Gln Gln Pro
 450 455 460

Val Asp Arg Lys Val
 465

<210> 9

<211> 1739

<212> DNA

<213> Mus musculus

<400> 9

atggatcttc taccceccaa gccgaagtac aaccacttc ggaatgagtc tctgtcatcg
 60

ctggaggagg gggcttcggg gtctaccct ccggaggagc tacctcccc atcagcttca
 120

tccctgggac ccattctgcc tcctctgccg ggggacgata gtccgactac cctgtgttcc
 180

ttctttcccc ggatgagcaa cctgaagctg gccaatcctg ctggggggcg cctggggcct
240

aaaggggagc caggaaaggc tgctgaagat ggggaaggga gtgcaggggc agcccttcgg
300

gactcaggcc tcttgccct cctccaggac atgaacaagc tgagtggagg cggcggggcg
360

aggactcggg tagaaggggg ccagctgggg ggcgaggagt ggaccagaca cgggagcttt
420

gtcaataagc ccacacgagg ctggctgcat cccaacgaca aagtcatggg acctgggggt
480

tcctacttgg ttcggtacat gggctgtgtg gaggtcttac agtcaatgcg agcccttgac
540

ttcaataccc ggactcaggt caccaggag gccatcagtt tgggtgtgtga agctgtgcct
600

gggtgccaaag gggcgacaag gaggagaaag ccttgtagcc gccactcag ctccatcctg
660

gggaggagta acctgaagtt tgctggaatg ccaatcactc tactgtgtc taccagcagc
720

cttaacctca tggcagccga ctgcaaacag atcattgcc accatcacat gcaatctatc
780

tctttcgct ccggtgggga tccggacaca gctgagtatg ttgcctatgt tgccaaagac
840

cctgtgaatc agagagcctg ccatactctg gagtgtcctg aagggttgc tcaggatgtc
900

atcagcacca tcgggcaggc ctttgagttg cgcttcaaac agtatctcag gaatccaccg
960

aagctggta ccccccata caggatggct ggctttgatg gctcagcttg ggatgaggag
1020

gaagaagagc ccctgacca tcagtactac aatgactttc cagggaagga acccctctt
1080

gggtggggtg tagatatgag gcttcgggaa ggggctgctc gaccactct gcctagtgc
1140

cagatgtcca gccacttggg agctacactg cctatagggc agcatgctgc aggagaccat
1200

gaagtccgta aacagatgtt gcctccgcg ccttgcccag gcagagaact cttcgatgac
1260

ccctcctatg tcaacatcca gaatctagac aaggcccggc aggctggggg tggggctggg
1320

ccccaaatc cttctcttaa tggcagtgc ccccgagacc tttttgacat gaagccctt
1380

gaagatgcac ttcgggtgcc acccccaccg cagtccatgt ccatggctga gcagctgcaa
1440

ggggagccct ggttcacagg gaagctgagc cggagggagg ccgaggcgct gctgcagctc
1500

aatggtgact tcttggtgcg agagagcacg accacgcctg gccagtatgt gctcactggc
1560

ctgcagagtg ggcagcccaa gcacttgctg ctggtggacc ctgaaggtgt ggttcggaca
1620

aaggatcacc gctttgagag tgtcagtcac ctgatcagct accacatgga caatcacttg
1680

cccatcatct ctgcgggcag cgaactgtgc ctacagcaac ccgtggatcg gaaagtgga
1739

<210> 10

<211> 579

<212> PRT

<213> Mus musculus

<400> 10

Met Asp Leu Leu Pro Pro Lys Pro Lys Tyr Asn Pro Leu Arg Asn Glu
1 5 10 15

Ser Leu Ser Ser Leu Glu Glu Gly Ala Ser Gly Ser Thr Pro Pro Glu
20 25 30

Glu Leu Pro Ser Pro Ser Ala Ser Ser Leu Gly Pro Ile Leu Pro Pro
35 40 45

Leu Pro Gly Asp Asp Ser Pro Thr Thr Leu Cys Ser Phe Phe Pro Arg
50 55 60

Met Ser Asn Leu Lys Leu Ala Asn Pro Ala Gly Gly Arg Leu Gly Pro
65 70 75 80

Lys Gly Glu Pro Gly Lys Ala Ala Glu Asp Gly Glu Gly Ser Ala Gly
85 90 95

Ala Ala Leu Arg Asp Ser Gly Leu Leu Pro Leu Leu Gln Asp Met Asn
100 105 110

Lys Leu Ser Gly Gly Gly Gly Arg Arg Thr Arg Val Glu Gly Gly Gln
115 120 125

Leu Gly Gly Glu Glu Trp Thr Arg His Gly Ser Phe Val Asn Lys Pro
130 135 140

Thr Arg Gly Trp Leu His Pro Asn Asp Lys Val Met Gly Pro Gly Val
145 150 155 160

Ser Tyr Leu Val Arg Tyr Met Gly Cys Val Glu Val Leu Gln Ser Met
165 170 175

Arg Ala Leu Asp Phe Asn Thr Arg Thr Gln Val Thr Arg Glu Ala Ile
180 185 190

Ser Leu Val Cys Glu Ala Val Pro Gly Ala Lys Gly Ala Thr Arg Arg
195 200 205

Arg Lys Pro Cys Ser Arg Pro Leu Ser Ser Ile Leu Gly Arg Ser Asn
210 215 220

Leu Lys Phe Ala Gly Met Pro Ile Thr Leu Thr Val Ser Thr Ser Ser
225 230 235 240

Leu Asn Leu Met Ala Ala Asp Cys Lys Gln Ile Ile Ala Asn His His
245 250 255

Met Gln Ser Ile Ser Phe Ala Ser Gly Gly Asp Pro Asp Thr Ala Glu
260 265 270

Tyr Val Ala Tyr Val Ala Lys Asp Pro Val Asn Gln Arg Ala Cys His
275 280 285

Ile Leu Glu Cys Pro Glu Gly Leu Ala Gln Asp Val Ile Ser Thr Ile
290 295 300

Gly Gln Ala Phe Glu Leu Arg Phe Lys Gln Tyr Leu Arg Asn Pro Pro
305 310 315 320

Lys Leu Val Thr Pro His Asp Arg Met Ala Gly Phe Asp Gly Ser Ala
325 330 335

Trp Asp Glu Glu Glu Glu Glu Pro Pro Asp His Gln Tyr Tyr Asn Asp
340 345 350

Phe Pro Gly Lys Glu Pro Pro Leu Gly Gly Val Val Asp Met Arg Leu
355 360 365

Arg Glu Gly Ala Ala Arg Pro Thr Leu Pro Ser Ala Gln Met Ser Ser
370 375 380

His Leu Gly Ala Thr Leu Pro Ile Gly Gln His Ala Ala Gly Asp His
 385 390 395 400

Glu Val Arg Lys Gln Met Leu Pro Pro Pro Pro Cys Pro Gly Arg Glu
 405 410 415

Leu Phe Asp Asp Pro Ser Tyr Val Asn Ile Gln Asn Leu Asp Lys Ala
 420 425 430

Arg Gln Ala Gly Gly Gly Ala Gly Pro Pro Asn Pro Ser Leu Asn Gly
 435 440 445

Ser Ala Pro Arg Asp Leu Phe Asp Met Lys Pro Phe Glu Asp Ala Leu
 450 455 460

Arg Val Pro Pro Pro Pro Gln Ser Met Ser Met Ala Glu Gln Leu Gln
 465 470 475 480

Gly Glu Pro Trp Phe His Gly Lys Leu Ser Arg Arg Glu Ala Glu Ala
 485 490 495

Leu Leu Gln Leu Asn Gly Asp Phe Leu Val Arg Glu Ser Thr Thr Thr
 500 505 510

Pro Gly Gln Tyr Val Leu Thr Gly Leu Gln Ser Gly Gln Pro Lys His
 515 520 525

Leu Leu Leu Val Asp Pro Glu Gly Val Val Arg Thr Lys Asp His Arg
 530 535 540

Phe Glu Ser Val Ser His Leu Ile Ser Tyr His Met Asp Asn His Leu
 545 550 555 560

Pro Ile Ile Ser Ala Gly Ser Glu Leu Cys Leu Gln Gln Pro Val Asp
 565 570 575

Arg Lys Val

<210> 11
 <211> 11
 <212> PRT
 <213> Artificial Sequence
 <220>

<223> RTK binding site variant

<400> 11

Leu	Pro	Val	Pro	Glu	Tyr	Ile	Asn	Gln	Ser	Val
1				5					10	

<210> 12

<211> 11

<212> PRT

<213> Artificial Sequence

<220>

<223> RTK binding site variant

<400> 12

Leu	Pro	Val	Pro	Glu	Phe	Ile	Asn	Gln	Ser	Val
1				5					10	

<210> 13

<211> 11

<212> PRT

<213> Artificial Sequence

<220>

<223> RTK binding site variant

<400> 13

Ile	Glu	Asn	Pro	Gln	Tyr	Phe	Ser	Asp	Ala	Cys
1				5					10	

<210> 14

<211> 11

<212> PRT

<213> Artificial Sequence

<220>

<223> RTK binding site variant

<400> 14

Ile	Glu	Asn	Pro	Gln	Phe	Phe	Ser	Asp	Ala	Cys
1				5					10	

<210> 15

<211> 11

<212> PRT

<213> Artificial Sequence

<220>

<223> RTK binding site variant

<400> 15

Ala Glu Asn Ala Glu Tyr Leu Arg Val Ala Pro
1 5 10 25

<210> 16
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> RTK variants

<400> 16

Asn Ala Thr Phe Val Asn Val Lys Cys
1 5